

SEQUENCE LISTING

<110> Merck & Co., Inc.

<120> HCV RNA-DEPENDENT RNA POLYMERASE

<130> 21471 PCT

<150> 60/535,708

<151> 2004-01-09

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> modified HCV NS5B

<400> 1

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					20			25				30			
Arg	Tyr	His	Asn	Lys	Val	Tyr	Cys	Thr	Thr	Thr	Lys	Ser	Ala	Ser	Leu
	35					40				45					
Arg	Ala	Lys	Lys	Val	Thr	Phe	Asp	Arg	Met	Gln	Val	Leu	Asp	Ser	Tyr
	50					55				60					
Tyr	Asp	Ser	Val	Leu	Lys	Asp	Ile	Lys	Leu	Ala	Ala	Ser	Lys	Val	Thr
	65				70			75			80				
Ala	Arg	Leu	Leu	Thr	Met	Glu	Glu	Ala	Cys	Gln	Leu	Thr	Pro	Pro	His
					85				90			95			
Ser	Ala	Arg	Ser	Lys	Tyr	Gly	Phe	Gly	Ala	Lys	Glu	Val	Arg	Ser	Leu
					100			105			110				
Ser	Gly	Arg	Ala	Val	Asn	His	Ile	Lys	Ser	Val	Trp	Lys	Asp	Leu	Leu
		115				120				125					
Glu	Asp	Ser	Glu	Thr	Pro	Ile	Pro	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu
	130				135				140						
Val	Phe	Cys	Val	Asp	Pro	Thr	Lys	Gly	Gly	Lys	Lys	Ala	Ala	Arg	Leu
	145				150				155			160			
Ile	Val	Tyr	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu
		165				170				175					
Tyr	Asp	Ile	Thr	Gln	Lys	Leu	Pro	Gln	Ala	Val	Met	Gly	Ala	Ser	Tyr
		180				185				190					
Gly	Phe	Gln	Tyr	Ser	Pro	Ala	Gln	Arg	Val	Glu	Phe	Leu	Leu	Lys	Ala
		195				200				205					
Trp	Ala	Glu	Lys	Lys	Asp	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys
	210				215				220						
Phe	Asp	Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile
	225				230				235			240			

Tyr Arg Ala Cys Ser Leu Pro Glu Glu Ala His Thr Ala Ile His Ser
 245 250 255
 Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly
 260 265 270
 Gln Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr
 275 280 285
 Ser Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys
 290 295 300
 Lys Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp
 305 310 315 320
 Leu Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn
 325 330 335
 Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
 340 345 350
 Asp Pro Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
 355 360 365
 Ser Asn Val Ser Val Ala Leu Gly Pro Gln Gly Arg Arg Arg Tyr Tyr
 370 375 380
 Leu Thr Arg Asp Pro Thr Thr Pro Ile Ala Arg Ala Ala Trp Glu Thr
 385 390 395 400
 Val Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr
 405 410 415
 Ala Pro Thr Ile Trp Ala Arg Met Val Leu Met Thr His Phe Phe Ser
 420 425 430
 Ile Leu Met Ala Gln Asp Thr Leu Asp Gln Asn Leu Asn Phe Glu Met
 435 440 445
 Tyr Gly Ala Val Tyr Ser Val Ser Pro Leu Asp Leu Pro Ala Ile Ile
 450 455 460
 Glu Arg Leu His Gly Leu Asp Ala Phe Ser Leu His Thr Tyr Thr Pro
 465 470 475 480
 His Glu Leu Thr Arg Val Ala Ser Ala Leu Arg Lys Leu Gly Ala Pro
 485 490 495
 Pro Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu
 500 505 510
 Ile Ser Arg Gly Arg Ala Ala Val Cys Gly Arg Tyr Leu Phe Asn
 515 520 525
 Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Arg
 530 535 540
 Leu Leu Asp Leu Ser Ser Trp Phe Thr Val Gly Ala Gly Gly Asp
 545 550 555 560
 Ile Tyr His Ser Val Ser Arg Ala Arg Pro Arg
 565 570

<210> 2

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> modified HCV NS5B

<400> 2

Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly
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Pro Glu Glu Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Met
 20 25 30
 Arg Phe His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu
 35 40 45
 Arg Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His
 50 55 60
 Tyr Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val Ser
 65 70 75 80
 Ala Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro Pro His
 85 90 95
 Ser Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu
 100 105 110
 Ser Arg Arg Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu
 115 120 125
 Glu Asp Gln His Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu
 130 135 140
 Val Phe Cys Ile Asp Pro Thr Lys Gly Gly Lys Lys Pro Ala Arg Leu
 145 150 155 160
 Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
 165 170 175
 Tyr Asp Ile Ala Gln Lys Leu Pro Lys Ala Ile Met Gly Pro Ser Tyr
 180 185 190
 Gly Phe Gln Tyr Ser Pro Ala Glu Arg Val Asp Phe Leu Leu Lys Ala
 195 200 205
 Trp Gly Ser Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
 210 215 220
 Phe Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile
 225 230 235 240
 Tyr Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser
 245 250 255
 Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly
 260 265 270
 Gln Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr
 275 280 285
 Ser Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys
 290 295 300
 Lys Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp
 305 310 315 320
 Leu Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn
 325 330 335
 Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
 340 345 350
 Asp Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
 355 360 365
 Ser Asn Val Ser Val Ala Leu Asp Ser Arg Gly Arg Arg Arg Tyr Phe
 370 375 380
 Leu Thr Arg Asp Pro Thr Thr Pro Ile Thr Arg Ala Ala Trp Glu Thr
 385 390 395 400
 Val Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr
 405 410 415
 Ala Pro Thr Ile Trp Val Arg Met Val Ile Met Thr His Phe Phe Ser
 420 425 430
 Ile Leu Leu Ala Gln Asp Thr Leu Asn Gln Asn Leu Asn Phe Glu Met
 435 440 445

Tyr Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile
 450 455 460
 Glu Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro
 465 470 475 480
 His Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro
 485 490 495
 Pro Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu
 500 505 510
 Ile Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn
 515 520 525
 Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser
 530 535 540
 Arg Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
 545 550 555 560
 Ile Tyr His Ser Val Ser His Ala Arg Pro Arg
 565 570

<210> 3
 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> modified HCV NS5B

<400> 3
 Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ser
 1 5 10 15
 Ala Glu Glu Glu Lys Leu Pro Ile Ser Pro Leu Ser Asn Ser Leu Leu
 20 25 30
 Arg His His Asn Leu Val Tyr Ser Thr Ser Ser Arg Ser Ala Ser Gln
 35 40 45
 Arg Gln Arg Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His
 50 55 60
 Tyr Lys Thr Ala Leu Lys Glu Val Lys Glu Arg Ala Ser Arg Val Lys
 65 70 75 80
 Ala Arg Met Leu Thr Ile Glu Glu Ala Cys Ala Leu Val Pro Pro His
 85 90 95
 Ser Ala Arg Ser Lys Phe Gly Tyr Ser Ala Lys Asp Val Arg Ser Leu
 100 105 110
 Ser Ser Arg Ala Ile Asp Gln Ile Arg Ser Val Trp Glu Asp Leu Leu
 115 120 125
 Glu Asp Thr Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
 130 135 140
 Val Phe Cys Val Asp Pro Ala Lys Gly Gly Arg Lys Pro Ala Arg Leu
 145 150 155 160
 Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Arg Ala Leu
 165 170 175
 Tyr Asp Val Ile Gln Lys Leu Ser Ile Glu Thr Met Gly Ser Ala Tyr
 180 185 190
 Gly Phe Gln Tyr Ser Pro Gln Gln Arg Val Glu Arg Leu Leu Lys Met
 195 200 205
 Trp Thr Ser Lys Lys Thr Pro Leu Gly Phe Ser Tyr Asp Thr Arg Cys
 210 215 220

Phe Asp Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile
 225 230 235 240
 Tyr Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser
 245 250 255
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 260 265 270
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 275 280 285
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 290 295 300
 Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
 305 310 315 320
 Leu Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala
 325 330 335
 Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
 340 345 350
 Asp Ala Pro Gln Pro Thr Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
 355 360 365
 Ser Asn Val Ser Val Ala Arg Asp Asp Lys Gly Arg Arg Tyr Tyr Tyr
 370 375 380
 Leu Thr Arg Asp Ala Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
 385 390 395 400
 Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr
 405 410 415
 Ala Pro Thr Ile Trp Val Arg Met Val Met Met Thr His Phe Phe Ser
 420 425 430
 Ile Leu Gln Ser Gln Glu Ile Leu Asp Arg Pro Leu Asp Phe Glu Met
 435 440 445
 Tyr Gly Ala Thr Tyr Ser Val Thr Pro Leu Asp Leu Pro Ala Ile Ile
 450 455 460
 Glu Arg Leu His Gly Leu Ser Ala Phe Thr Leu His Ser Tyr Ser Pro
 465 470 475 480
 Val Glu Leu Asn Arg Val Ala Gly Thr Leu Arg Lys Leu Gly Cys Pro
 485 490 495
 Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
 500 505 510
 Ile Ala Gln Gly Gly Lys Ala Lys Ile Cys Gly Leu Tyr Leu Phe Asn
 515 520 525
 Trp Ala Val Arg Thr Lys Thr Asn Leu Thr Pro Leu Pro Ala Thr Gly
 530 535 540
 Gln Leu Asp Leu Ser Ser Trp Phe Thr Val Gly Val Gly Gly Asn Asp
 545 550 555 560
 Ile Tyr His Ser Val Ser Arg Ala Arg Thr Arg
 565 570

<210> 4
 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> modified HCV NS5B

<400> 4

Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Val Thr Pro Cys Ala
 1 5 10 15
 Ala Glu Glu Ser Lys Leu Pro Ile Ser Pro Leu Ser Asn Ser Leu Leu
 20 25 30
 Arg His His Asn Met Val Tyr Ala Thr Thr Arg Ser Ala Val Thr
 35 40 45
 Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Val Asp Ser His
 50 55 60
 Tyr Asn Glu Val Leu Lys Glu Ile Lys Ala Arg Ala Ser Arg Val Lys
 65 70 75 80
 Ala Arg Leu Leu Thr Thr Glu Glu Ala Cys Asp Leu Thr Pro Pro His
 85 90 95
 Ser Ala Arg Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Ser His
 100 105 110
 Ser Arg Lys Ala Ile Asn His Ile Ser Ser Val Trp Lys Asp Leu Leu
 115 120 125
 Asp Asp Asn Asn Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
 130 135 140
 Val Phe Ala Val Asn Pro Ala Lys Gly Gly Arg Lys Pro Ala Arg Leu
 145 150 155 160
 Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Arg Ala Leu
 165 170 175
 His Asp Val Ile Lys Lys Leu Pro Glu Ala Val Met Gly Ala Ala Tyr
 180 185 190
 Gly Phe Gln Tyr Ser Pro Ala Gln Arg Val Glu Phe Leu Leu Thr Ala
 195 200 205
 Trp Lys Ser Lys Lys Thr Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
 210 215 220
 Phe Asp Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val
 225 230 235 240
 Tyr Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala
 245 250 255
 Leu Thr Asp Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly
 260 265 270
 Asp Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr
 275 280 285
 Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Ile
 290 295 300
 Arg Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp
 305 310 315 320
 Leu Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Asn Arg Ala
 325 330 335
 Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
 340 345 350
 Asp Ala Pro Gln Pro Ala Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
 355 360 365
 Ser Asn Val Ser Val Ala His Asp Val Thr Gly Lys Lys Val Tyr Tyr
 370 375 380
 Leu Thr Arg Asp Pro Glu Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
 385 390 395 400
 Val Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Val Tyr
 405 410 415
 Ala Pro Thr Ile Trp Val Arg Met Ile Leu Met Thr His Phe Phe Ser
 420 425 430

Ile Leu Gln Ser Gln Glu Ala Leu Glu Lys Ala Leu Asp Phe Asp Met
 435 440 445
 Tyr Gly Val Thr Tyr Ser Ile Thr Pro Leu Asp Leu Pro Ala Ile Ile
 450 455 460
 Gln Arg Leu His Gly Leu Ser Ala Phe Thr Leu His Gly Tyr Ser Pro
 465 470 475 480
 His Glu Leu Asn Arg Val Ala Gly Ala Leu Arg Lys Leu Gly Val Pro
 485 490 495
 Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
 500 505 510
 Ile Ala Gln Gly Arg Ala Lys Ile Cys Gly Ile Tyr Leu Phe Asn
 515 520 525
 Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Ala Ala Ala
 530 535 540
 Lys Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
 545 550 555 560
 Ile Tyr His Ser Met Ser His Ala Arg Pro Arg
 565 570

<210> 5
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> modified HCV NS5B

<400> 5
 Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
 1 5 10 15
 Ala Glu Glu Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Ile
 20 25 30
 Arg His His Asn Met Val Tyr Ser Thr Ser Arg Ser Ala Ser Leu
 35 40 45
 Arg Gln Lys Lys Val Thr Phe Asp Arg Val Gln Val Phe Asp Gln His
 50 55 60
 Tyr Gln Glu Ile Leu Lys Glu Ile Lys Leu Arg Ala Ser Lys Val Gln
 65 70 75 80
 Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Asp Leu Thr Pro Ser His
 85 90 95
 Ser Ala Arg Ser Lys Tyr Gly Tyr Gly Ala Gln Asp Val Arg Ser His
 100 105 110
 Ala Ser Lys Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu
 115 120 125
 Glu Asp Ser Asp Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
 130 135 140
 Val Phe Cys Val Asp Pro Ser Lys Gly Gly Arg Lys Pro Ala Arg Leu
 145 150 155 160
 Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
 165 170 175
 Tyr Asp Val Thr Gln Lys Leu Pro Gln Ala Val Met Gly Ser Ala Tyr
 180 185 190
 Gly Phe Gln Tyr Ser Pro Thr Gln Arg Val Glu Tyr Leu Leu Lys Met
 195 200 205

Trp Arg Ser Lys Lys Val Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
 210 215 220
 Phe Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Asn Asp Ile
 225 230 235 240
 Tyr Gln Ser Cys Gln Leu Asp Pro Val Ala Arg Arg Ala Val Ser Ser
 245 250 255
 Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Val Asn Ser Lys Gly
 260 265 270
 Gln Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 275 280 285
 Ser Met Gly Asn Thr Ile Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys
 290 295 300
 Arg Ala Ala Asn Ile Lys Asp Cys Asp Met Leu Val Cys Gly Asp Asp
 305 310 315 320
 Leu Val Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Thr Glu Ser
 325 330 335
 Leu Arg Ala Phe Thr Asp Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
 340 345 350
 Asp Ala Pro Gln Pro Thr Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
 355 360 365
 Ser Asn Val Ser Val Ala His Asp Gly Asn Gly Lys Arg Tyr Tyr Tyr
 370 375 380
 Leu Thr Arg Asp Cys Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
 385 390 395 400
 Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Phe
 405 410 415
 Ala Pro Thr Ile Trp Val Arg Met Val Leu Met Thr His Phe Phe Ser
 420 425 430
 Ile Leu Gln Ser Gln Glu Gln Leu Glu Lys Ala Leu Asp Phe Asp Ile
 435 440 445
 Tyr Gly Val Thr Tyr Ser Val Ser Pro Leu Asp Leu Pro Ala Ile Ile
 450 455 460
 Gln Arg Leu His Gly Met Ala Ala Phe Ser Leu His Gly Tyr Ser Pro
 465 470 475 480
 Val Glu Leu Asn Arg Val Gly Ala Cys Leu Arg Lys Leu Gly Val Pro
 485 490 495
 Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
 500 505 510
 Ile Ala Gln Gly Lys Ala Ala Ile Cys Gly Lys Tyr Leu Phe Asn
 515 520 525
 Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Val Ser Ala Ser
 530 535 540
 Lys Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Asp Gly Gly Asp
 545 550 555 560
 Ile Tyr His Ser Val Ser Gln Ala Arg Pro Arg
 565 570

<210> 6
 <211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 1

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accacaacaa agagcgccctc actaagggtc aaaaaggtaa cttttgatag gatgcaagtg 180
ctcgactcct actacgactc agtcttaaag gacattaagc tagcggcctc caaggtcacc 240
gcaaggctcc tcaccatgga ggaggcttgc cagttAACcc caccggcattc tgcaagatct 300
aaatatgggt ttggggctaa ggaggcttgc agcttgcgt ggagggccgt taaccacatc 360
aagtccgtgt ggaaggaccc cctggaggac tcagaaacac caattccac aaccattatg 420
gccaaaaatg aggtgttctg cgtggacccc accaaggggg gcaagaaagc agtcgcctt 480
atcgtttacc ctgacccctgg cgtcagggtc tgcgagaaga tggcccttta tgacattaca 540
caaaaacttc ctcaggcggt gatgggggt tcttatggat tccagtattc ccccgctcag 600
cggttagagt ttctctgaa agcatggcg gaaaagaagg accctatggg ttttcgtat 660
gatacccgat gctttgactc aaccgtcact gagagagaca tcaggactga ggagtccata 720
tatcgggctt gctccttgcc cgaggaggcc cacactgcca tacactcgct aactgagaga 780
cttacgtgg gagggttat gttcaacagc aaggccaaa cctgcgggta caggcgttgc 840
cgcccgccagcg ggggtgcac cactagcatg gggAACACCA tcacatgcta cgtgaaagcc 900
tttagccgtt gtaaagctgc agggataatc ggcgcaccaa tgctggatg cggcgatgac 960
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gttagacact cccctgtcaa ttcatggctg ggaaacatca tccagtacgc cccgaccata 1260
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tggaaagagcc gggcacgtgc agtcagggtc tccctcatct cccgtggggg gagagcggcc 1560
gtctcggtc gatatctctt caactgggtc gtgaagacca agctcaaact cactccattg 1620
ccggaggcgcc gcctccctgga ttatccagc tggttcaccg tcggcgccgg cggggcgac 1680
attatcaca gcgtgtcgcg tgcccgacca cgc 1713

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<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 2

<400> 7

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acaacctcaa ggagtgcctc tctgagggca aagaagggtg cttttgacag ggtgcaggtg 180
ctggacgcac actatgactc agtctgcag gacgttaagc gggccgcctc taagggttagt 240
gcaaggctcc tcacggtaga ggaaggctgc ggcgtgaccc cgcggccactc cgccaaatcg 300
cgatacggat ttggggccaa agaggtgcgc agcttatacca ggagggccgt taaccacatc 360
cggtccgtgt gggaggaccc cctggaaagac caacataaccc caattgacac aactatcatg 420
gctaaaaatg aggtgttctg cattgatcca actaaagggtg gaaaaaaagcc agtcgcctc 480
atcgatatacc cccgacccctgg ggtcagggtt tgcgaaaaga tggcccttta tgacatcgca 540
caaaaagcttc ccaaaggcgat aatggggcca tcctatgggt tccaaatactc tcccgccagaa 600
cggtcgttccaa agcttggggg agtaagaagg acccaatggg gtttcgtat 660
gacaccgcgt gctttgactc aaccgtcact gagagggaca taagaacaga agaattccata 720
tatcaggctt gttctctgcc tcaagaaggcc agaactgtca tacactcgct cactgagaga 780
cttacgttag gagggtccat gacaaacagc aaaggccat cctgcggcta caggcgttgc 840
cgcccaagcg gtttttcac caccagcatg gggaaatcca tgacatgta catcaaagcc 900

cttgcagcgt gtaaggctgc agggatcgta gaccctgtta tgttgggttg tggagacgac 960
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 acggaggcta tgaccaggtt ttccgccccct cccgggtgacc ttcccagacc ggaatatgac 1080
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 cgccggtaact tcctaaccag agaccctacc actccaatca cccgagctgc ttgggaaaca 1200
 gtaagacact cccctgtcaa ttcttggctg ggcaacatca tccagtagcgc ccccacaatc 1260
 tgggtccgga tggtcataat gactcaactt ttctccatac tattggccca ggacactctg 1320
 aaccaaaatc tcaatttga gatgtacggg gcagttactt cggtcaatcc attagaccta 1380
 ccggccataa ttgaaaggct acatgggctt gaaggctttt cactgcacac atactctccc 1440
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 tggaaagagtc gggcgcgtgc cgtgagagct tcactcatcg cccaaaggagc gagggcggcc 1560
 atttgtggcc gctacccctt caactgggctg gtgaaaacaa agctcaaact cactccattg 1620
 cccgaggcga gccgcctgga ttatccggg tggttcaccg tggcgcggc cggggcgcac 1680
 atttacaca gcgtgtcgca tgcccgaccc cgc 1713

<210> 8

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 3

<400> 8

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 acgtcgctga gaagcgcttc ccagcgctcg aggaaaggta ccttcgacag actgcaggtg 180
 ctcgacgacc attataagac tgcattaaag gaggtgaagg agcgagcgctc tagggtaag 240
 gcccgcatgc tcaccatcgaa ggaagcgtgc gcgctcgctc ctccctcaactc tgcccggtcg 300
 aagttcggtt atagtgcgaa ggacgttcgc tccttgcataa gcagggccat tgaccagatc 360
 cgctccgtct gggaggaccc gctggaagac accacaactc caattccaaac caccatcatg 420
 gcgaagaacg aggtgtttt gttggacccc gctaaagggg gccgcgaagcc cgctcgccctc 480
 atttgttacc ctgaccccttggg ggtgcgtgtc tggatggaaac gcccctata tgacgtgata 540
 cagaagttgtt caattgagac gatgggttcc gcttatggat tccaaatactc gcctcaacag 600
 cgggtcgaaac gtctactgaa gatgtggacc tcaaagaaaa ccccttggg gttctcatat 660
 gacaccgcgt gctttgactc aactgtcactt gaacaggaca tcagggtaga agaggagata 720
 tatcaatgtt gtaacccatgtt accggaggccc agggaaatgtt ttcctccctt cacggagccgg 780
 ctttactgtcg gggcccttat gttcaacagc aaggggggccc agtgtggta tcgcccgttgc 840
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 acagcggcccg cgaaggccgc aggccctccgg aaccggact ttctcgctcg cggagatgtat 960
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 aggtattttt accttcaccccg tgatgccact actcccttag ccccgccggc ttgggaaaca 1200
 gcccgtcaca ctccagtcaa ctccctggta ggtaacatca tcatgtacgc gcctactatc 1260
 tgggtcgca tggtaatgtt gacacacttt ttctccatac tccaaatccca ggagataactt 1320
 gatcgacccccc ttgactttgtt aatgtacggg gccacttact ctgtcactcc gctggattta 1380
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 tggagacatc gggcgcggc agtgcgcgc aagcttacg cccaggggagg gaaggccaaa 1560
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 ccagccactg gccagttgga ctgtccagc tggtttacgg ttgggtgtcg cgggaacgac 1680
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<210> 9

<211> 1713
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence encoding SEQ ID NO: 4

<400> 9

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 acgaccaccc gttctgctgt gacacggcag aagaaggta ccttcgaccg cctgcagggtg 180
 gtggacagtc actacaatga agtgcttaag gagataaagg cacgagcatc cagagtgaag 240
 gcacgcttgc ttaccacaga ggaagcttgc gacctgacgc ccccccactc agccagatca 300
 aagttcggct acggggcgaa ggatgttcgg agccattccc gcaaggccat taaccacatc 360
 agctccgtgt ggaaggactt gctggacgac aacaataccc caataccaaac aacaatcatg 420
 gccaaaaatg aggtcttcgc tggtaaccct ggcgaaggag gtcggaagcc tgctcgccctg 480
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 aaaaaactgc ctgaggccgt gatgggagcc gcttatggct tccaaatactc cccagcgcag 600
 cgggtggaat ttcttcgtac tgcttggaaag tcgaagaaga ccccaatggg gttcttttat 660
 gatacccgt gctttgactc cactgttaacc gaaaaggaca tcagggtcga ggaagaggtc 720
 tattcgtgtt gtgaccttgg gcccgaagcc cgcaaaagtca tcaccgcctt cacagataga 780
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 atatgtggca tataccctt taactgggac gtaaaaaacca aactcaaact cactccattt 1620
 cctgcccgtg ccaaactcga ttatcggtt tggttacgg taggcgcggc cgggggagac 1680
 atttattcaca gcatgtctca tgcccgaccc cgc 1713

<210> 10
 <211> 1713
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence encoding SEQ ID NO: 5

<400> 10

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 accacatcac gcagcgcggcag cttccgcgg aagaaggta catttgcacag agtgcaagtg 180
 ttgcaccaac attaccagga aatactaaag gagattaagc ttgcagcgtc caaggtgcag 240
 gcgaagctt tattccgtaga ggaagccctc gacccacac catcgacactc agcccggtcc 300
 aaatatgggt atgggtgcaca ggacgtttaga agccatgcta gcaaggccgt caaccacatc 360
 cgctccgtgt gggaggactt gctagaagac tctgataactc caattccac aaccatcatg 420
 gctaaagaatg aagtcttcgtc cgtatgatccg tcgaagggtg gacgcaagcc ggcacgctt 480

atattttacc cagacttggg cgtgcgggtc tgcgagaaga tggccctata cgacgtcacg 540
 cagaaggtaac cacaggccgt gatgggttca gcatacggat tccagtactc ccccacccag 600
 agggtttagt acctgtctcaa aatgtggcgg tcaaagaagg tgcctatggg cttttcttac 660
 gacaccaggt gttttgattc aaccgtcaact gagcgggaca tccggactga gaacgacatc 720
 tatacgatctt gccagctgga tcccgtagca aggagggcag tatcatccct aacggaacgg 780
 ctctacgttag gcccccccat ggtgaactcc aaggagacagt catgtggcta ccgtagatgc 840
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 tggagacatc gagccagagc tgtagagcc aaactcattt cccaaaggggg gaaagcggcc 1560
 atatgc当地 gta agtacccttt taactgggca gtgaagacca aactaaaact cactccattt 1620
 gtc当地 cgc当地 gcaaggcttga ctatcaggc tggttcgtgg ccggctacga cgggggggac 1680
 atttatacaca gcgtgtccca ggctcgaccc cgt 1713

<210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 11
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<210> 12
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 12
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34

<210> 13
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 <212> DNA
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<220>
 <223> Primer

<400> 13
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23

<210> 14
<211> 24
<212> DNA
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<220>
<223> Primer

<400> 14
gtgccgctct atcgagcggg gagt

24

<210> 15
<211> 21
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<220>
<223> Primer

<400> 15
atactcctgg acagggggccc t

21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
atactcctgg acagggggccc t

21

<210> 17
<211> 21
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<220>
<223> Primer

<400> 17
ccgctctacc gagcggggag t

21

<210> 18

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
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24

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
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30

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
ccagctcacc gtgctggcag g

21

<210> 21
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
gatcggagga cgtcggtgc tgtt

24

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
gttcgatgtc atactcggtt actg

24

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
aagctgccta ccgagcaggc agca

24

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
ctaagctcag gctcttggtc cact

24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
gacgacgtcg tatgttgttc catg

24

<210> 26
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
ctaccgagcg gggagcaaaa agatg

25

<210> 27
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> His-Tag

<400> 27
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<210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence encoding SEQ ID NO: 27

<400> 28
ctcgagcacc accaccacca ccac

24